

Different Responses of Macrophages to Smooth and Rough *Brucella* spp.: Relationship to Virulence

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By comparing smooth wild-type *Brucella* strains to their rough mutants, we show that the lipopolysaccharide (LPS) O side chain of pathogenic *Brucella* has a dramatic impact on macrophage activation. It favors the development of virulent *Brucella* by preventing the synthesis of immune mediators, important for host defense. We conclude that this O chain property is firmly linked to *Brucella* virulence.

The genus *Brucella* is a gram-negative, facultative, intracellular pathogen that produces diseases in different mammals, including humans. As in other gram-bacteria, the lipopolysaccharide (LPS) of *Brucella* is an important component of the outer membrane (3, 7), but its precise role in the biology of the pathogen is still an unsolved issue. In smooth pathogenic *Brucella* spp. (*B. abortus*, *B. suis*, and *B. melitensis*), lipopolysaccharide (LPS) has been implicated in bacterial virulence. This proposal is based on the observation that rough mutants derived from these strains are greatly attenuated in animals or isolated macrophages compared to parental *Brucella* (1, 10, 13, 18, 33, 36, 37, 40). The rough mutants thus appear to act as a putative live vaccine. Their attenuation is mainly explained by the properties of the LPS O side chain, a long linear homopolymer of α 1,2-linked perosamine (5). The O chain appears to be a key molecule for invasion and development (35) and protection from apoptosis (14). It also protects the bacteria from cellular cationic peptides (16, 32), oxygen metabolites (39), and complement-mediated lysis (13, 30). Recently, it was observed that the O chain also impairs cytokine production in infected human macrophages, and it was postulated that this could be a way for the pathogen to control host defense (37). We have analyzed this possibility in a murine model of infection commonly used to compare the levels of virulence of *Brucella* strains.

B. melitensis B3B2 (18) and R5 (Table 1) and *B. suis* manb (15) are three rough mutants of wild-type *B. melitensis* 16M and *B. suis* 1330, respectively: these mutants are attenuated in BALB/c mice compared to parental *Brucella* (9) (Table 1). Their ability to infect murine macrophage-like cells was assessed by using J774A.1 cells cultured in 24-well plates (10^6 cells per well). These cells were incubated at 37°C for 30 min with a bacterial suspension (multiplicity of infection [MOI] = 40) (21, 40). After three washes, the infected macrophages were reincubated in 1 ml of RPMI–10% fetal calf serum (FCS) supplemented with 30 μ g of gentamicin/ml for at least 40 min to kill extracellular bacteria. At several intervals postinfection (p.i.), cells were washed and lysed in 0.2% Triton X-100. The

number of viable intracellular bacteria (CFU per well) was determined by plating serial 10-fold dilutions onto Trypticase soy agar (TSA) plates. Figure 1 indicates that rough *B. melitensis* strains R5 and B3B2 were respectively phagocytosed 500- and 100-fold more than smooth *B. melitensis* strain 16M ($P < 0.005$ for each mutant versus *B. melitensis*) and that *B. suis* manb was internalized 50-fold more than *B. suis* 1330 ($P < 0.003$). As reported previously (18, 21, 24), after a short period of decrease, the number of intracellular *B. suis* and *B. melitensis* cells significantly increased. At 48 h p.i., there were 100- to 1,000-fold more intracellular smooth bacteria than were found at the onset of infection. In contrast, intracellular rough mutants were eliminated, and depending on the mutant analyzed, there were 10^2 - to 10^3 -fold-fewer intracellular bacteria at 48 h p.i. than after phagocytosis. All of the rough mutants were eliminated, albeit with different kinetics, which can be explained by the genetic background of the mutants. The elevated invasion of the rough mutants was possibly due to the exposure of ligands that are normally hidden by the O chain and the consequent increased capacity of rough *Brucella* to adhere to macrophages (11, 37). Entry of smooth and rough *Brucella* strains into the cells through different pathways (35) could also involve receptors with a distinct ability to regulate the levels of phagocytosis. Because rough *Brucella* strains are efficiently internalized (10, 11, 17, 35), the bacteria could alter the plasma membrane, causing cell damage. Cell toxicity could also have resulted from induction of cell apoptosis, because rough *Brucella* strains do not protect macrophages from exogenous apoptotic signals (14), unlike smooth *Brucella* strains (23). However, under our experimental conditions (MOI of 40, presence of serum, no exogenous apoptotic signals, 48 h of culture), the lactate dehydrogenase activities of supernatants (measured as described in reference 22) were similar in cells infected by rough or smooth *Brucella* strains (data not shown). This indicates that elimination of the rough mutant did not result from cell toxicity and release of bacteria in the gentamicin-supplemented medium. Therefore, as postulated (37), the observed fate of rough *Brucella* strains could have resulted from a cellular response triggered by the bacteria. The macrophage response to different *Brucella* was assessed by measuring the expression of inducible nitric oxide synthase (iNOS), tumor necrosis factor alpha (TNF- α), interleukin-1 (IL-1), IL-

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TABLE 1. *Brucella* strains used in the study

Strain	Genotypic and/or phenotypic description ^a	No. of CFU/ spleen at 3 wk p.i. ^b
<i>B. melitensis</i>		
16M	Spontaneous smooth nalidixic acid-resistant mutant of <i>B. melitensis</i> 16M, (41)	>10 ⁴
R5	Natural rough mutant of <i>B. melitensis</i> 16M (SIA-DGA collection, Zaragoza, Spain)	<10
B3B2	Rough mini-Tn5 insertion mutant of <i>B. melitensis</i> 16M with the perosamine synthase gene deleted, kanamycin resistant (18)	<10
<i>B. suis</i>		
1330	Smooth wild-type <i>B. suis</i> (ATCC 23444)	>5 × 10 ⁵
manb	Rough mini-Tn5 insertion mutant of <i>B. suis</i> 1330 with the phosphomannose gene deleted, kanamycin resistant (15)	<10
GFP	Smooth ampicillin-resistant mutant of <i>B. suis</i> 1330 that constitutively expresses the GFP gene (32)	>5 × 10 ⁵

^a The smooth and rough phenotypes of the different *Brucella* strains were assessed by crystal violet staining and verified by immunoblotting techniques involving monoclonal antibodies that recognize the smooth or rough LPS of *Brucella* (8).

^b BALB/c mice were injected intraperitoneally with 5 × 10⁴ CFU of *B. suis* 1330 or manb or of *B. melitensis* 16M, B3B2, or R5. Six mice per group were killed by CO₂ asphyxiation 3 weeks post-inoculation. Spleens were aseptically removed and homogenized with 10 ml of phosphate-buffered saline to determine *Brucella* counts (CFU per spleen) as indicated in references 28 and 29.

10, IL-12, MIP-2, and KC (CXC chemokine, murine homologue of GRO- α) mRNAs in cells infected for 5 h. Expression of mRNAs was determined by reverse transcription-PCR (RT-PCR) under the conditions described in our previous studies (20, 21). The primers, mRNA and cDNA preparations, and procedures used for normalization of amplicon intensities have been described elsewhere in detail (20, 21, 24). The inflammatory cytokine and iNOS transcripts that are not expressed in quiescent cells were strongly induced when the invasive agent was one of the rough bacteria, but not when *B. suis* or *B. melitensis* 16M was used. This indicated that rough *Brucella* strains triggered an activation process that did not occur in smooth *Brucella* strain-infected cells. The transcripts were expressed at levels comparable to those occurring in quiescent cells stimulated with 100 ng of *Escherichia coli* LPS per ml. TNF- α and NO are two products of macrophage response directly involved in killing of intracellular *Brucella* (2, 9, 21, 42, 43); their production was measured in infected cell supernatants as described in reference 21. A significant accumulation of NO₂⁻ (the end product of NO) and TNF- α was observed in supernatants of all rough *Brucella* strain-infected cells. The accumulation of NO was time dependent for at least 48 h p.i. and was similar to that induced by the combination of *E. coli* LPS with gamma interferon (IFN- γ) (Table 2) (21). The TNF- α concentration, optimal at 24 h, varied from 10 to 28 ng/ml, depending on the rough mutant. In accordance with previous reports (12, 21, 41), macrophages invaded by smooth *Brucella* strains did not express iNOS nor release any NO (Table 2). They produced relatively weak amounts of TNF- α , the cytokine concentration in supernatants remaining around 0.5 ng/ml (Table 2), which in each case was significantly lower than that induced by each of the rough bacterial strains assessed. Several studies have clearly demonstrated an inverse

correlation between TNF- α release and the invasive capacity of *Brucella* (reviewed in reference 2). Moreover, NO which is deleterious to *Brucella* (28), was produced in rough *Brucella* strain-infected cells but not in smooth *Brucella* strain-infected cells. Besides TNF- α and NO, IL-1 is an important mediator of *Brucella* development (27), and the phagolysosomal destruction of microorganisms commonly corresponds to high levels of cytokine production (34). KC and MIP-2 have antibacterial properties in vivo by attracting neutrophils to the site of infection (24, 34), and IL-12 is a necessary factor for the establish-

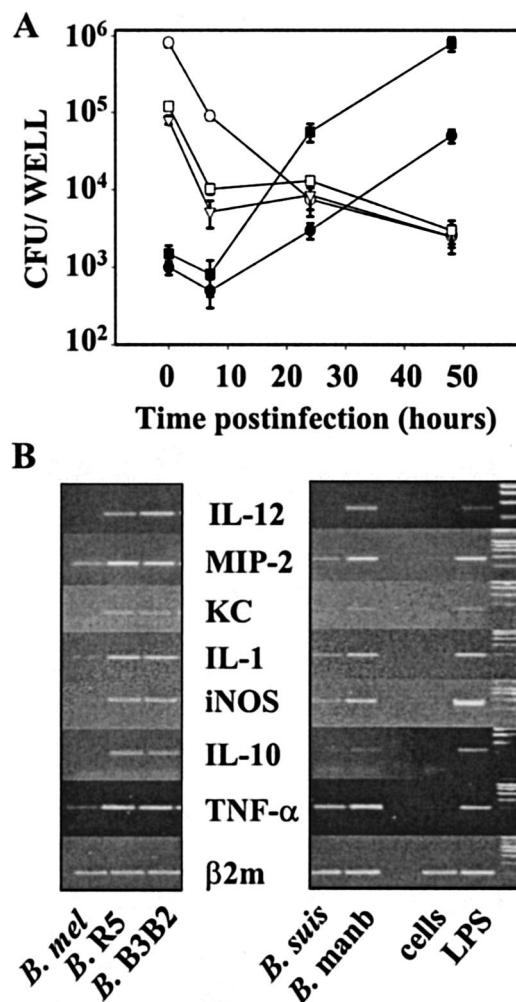


FIG. 1. (A) Infection of J774.A1 cells by different smooth and rough strains of *Brucella*. J774.A1 cells were infected (MOI = 40) with *B. suis* (■), *B. suis* manb (□), *B. melitensis* 16M (●), *B. melitensis* B3B2 (○), or *B. melitensis* R5 (△), and the intracellular fate of the bacteria was evaluated. The data presented are means \pm standard deviations of triplicate plate counts and are representative of three different experiments. (B) Cytokine and iNOS mRNA expression in *Brucella*-infected cells. The gene expression of different cytokines or iNOS was analyzed by RT-PCR performed on mRNAs of J774.A1 cells infected for 5 h and compared to gene expression in control cells (cells) or in cells induced with 100 ng/*E. coli* LPS/ml. The housekeeping gene coding for β 2-microglobulin was used as a standard (31). Cells were infected with *B. melitensis* 16M, R5, or B3B2 or *B. suis* 1330 or manb. Data are representative of three different experiments. The mRNAs and cDNA preparations, primers, and method used to compare amplicon intensities have been described elsewhere in detail (28, 31).

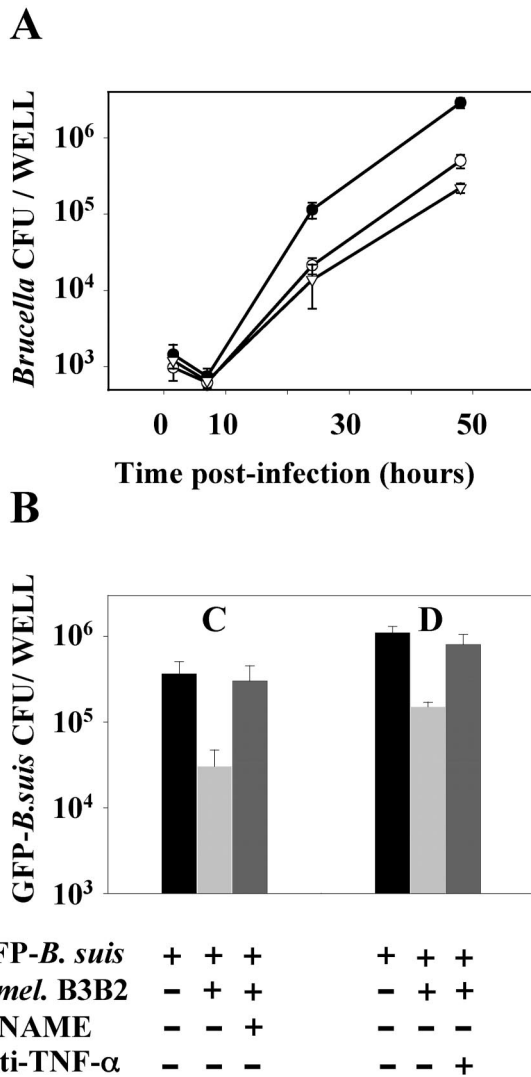


FIG. 2. (A) Intracellular development of *B. suis* GFP (CFU per well) in macrophages infected with *B. suis* GFP or coinfecting with *B. suis* GFP and a rough mutant of *Brucella*. J774.A1 cells (10⁶/well) were infected with *B. suis* GFP (MOI = 40) (●) or coinfecting with *B. suis* GFP and *B. suis* manb (○) or *B. suis* GFP and *B. melitensis* B3B2 (▽) (MOI = 40 for each bacteria). Infections were performed in triplicate. At different periods of time, the cells were lysed and the number of intracellular *B. suis* GFP cells was determined by plating the cell lysates on agar plates supplemented with ampicillin and expressed in CFU per well \pm standard deviation. At 48 h p.i., in four different experiments, the number of *B. suis* GFP cells in macrophages infected with only *B. suis* GFP was significantly higher than the number of *B. suis* GFP cells in macrophages coinfecting with *B. suis* GFP and *B. suis* manb ($P < 0.05$) or with *B. suis* GFP and *B. melitensis* B3B2 ($P < 0.01$). (B) Effect of NO and TNF- α on the development of *B. suis* in J774.A1 cells coinfecting with *B. suis* and *B. melitensis* B3B2. J774.A1 cells (10⁶/well) were infected with *B. suis* GFP (MOI = 40) or coinfecting with *B. suis* GFP and *B. melitensis* B3B2 (MOI = 40, for each bacteria). After the phagocytosis step (i.e., at the same time as gentamicin), L-NAME (3 mM) or the blocking anti-TNF- α antibody (5 μ g/ml) was added (or not) to the infected cultures. Infections were performed in triplicate. Forty-eight hours later, the intracellular number of *B. suis* GFP cells was determined for each condition and expressed as CFU per well \pm standard deviation. Experiments C and D were performed separately and repeated four times. The numbers of *B. suis* GFP cells phagocytosed in 30 min were as follows: 1,200 \pm 400 (inoculum of *B. suis* GFP) and 1,500 \pm 200 (inoculum of *B. suis* GFP and *B. melitensis* B3B2) for experiment C and 2,200 \pm 500 (inoculum

TABLE 2. NO₂⁻ and TNF- α production in J774.A1 cells infected with different strains of *Brucella* or coinfecting with *B. suis* GFP and a *Brucella* rough mutant

Infection ^a	Production of ^b :	
	NO ₂ ⁻ at 48 h (μM)	TNF-α at 24 h (ng/ml)
<i>B. suis</i> 1330	1.9 \pm 0.5*	0.7 \pm 0.5*
<i>B. suis</i> manb	27.7 \pm 1.7†‡	28.7 \pm 1.5†‡
<i>B. melitensis</i> 16M	3.0 \pm 1.1*	0.5 \pm 0.3*
<i>B. melitensis</i> R5	22.0 \pm 3.7§	10.0 \pm 2.7§
<i>B. melitensis</i> B3B2	16.3 \pm 3.7§	30.7 \pm 1.4‡§
<i>B. suis</i> GFP	2.3 \pm 0.5*	0.5 \pm 0.2*
<i>B. suis</i> GFP + manb	24.8 \pm 0.9	24.9 \pm 5.3
<i>B. suis</i> GFP + <i>B. melitensis</i> B3B2	18.2 \pm 3.7	27.8 \pm 2.5
<i>E. coli</i> LPS + IFN-γ	43.2 \pm 3.1‡	37.5 \pm 3.1‡
None	0.2 \pm 0.2	0.7 \pm 0.4

^a J774.A1 cells (10⁶/well) were infected (or not) with different smooth or rough *Brucella* strains (MOI = 40) or cultured with 100 ng of *E. coli* LPS plus 2 U of mouse recombinant IFN-γ per ml. In parallel experiments, cells were infected with *B. suis* GFP (MOI = 40) in the absence or presence of *B. suis* manb (or *B. melitensis* B3B2) (MOI = 40). At the indicated periods of time, cell supernatants were harvested and their NO₂⁻ or TNF- α contents were determined (21). The data presented are means \pm standard deviations of three different experiments. Comparisons between different assays were performed by using unpaired Student's *t* tests.

^b *, not significant compared to nontreated cells; †, $P < 0.001$ compared to *B. suis* 1330; ‡, $P < 0.001$ compared to nontreated cells; §, $P < 0.001$ compared to *B. melitensis* 16M; ||, $P < 0.001$ compared with values obtained in infections with *B. suis* GFP alone.

ment of the Th1 response, which in vivo determines the elimination of *Brucella* (44). If IL-10 is detrimental to the cells, it is also an anti-inflammatory molecule that controls the damaging effect of proinflammatory cytokines.

Therefore, in rough *Brucella* strain infection, the high production of TNF- α and NO concentration and possibly that of other effectors may mount a potent inflammatory response that imbalances the macrophage defense mechanisms to an extent favorable to the host cells. Conversely, smooth *Brucella* strains could be virulent in part because they induce little or no macrophage response, the LPS O chain limiting this response. To confirm this possibility, J774.A1 macrophages were coinfecting with smooth and rough *Brucella* strains, and the proliferation of the smooth bacteria was measured. J774.A1 cells (10⁶/ml/well) were simultaneously incubated at 37°C with *B. suis* GFP (an ampicillin-resistant mutant of *B. suis* 1330 that expresses the green fluorescent protein [GFP] gene) instead of *B. suis* (MOI = 40) (31) and a rough strain of *Brucella* (*B. suis* manb or *B. melitensis* B3B2) (MOI = 40) for 30 min. The protocol commonly used for infection (Fig. 1) (washing, cultures grown in RPMI-FCS with gentamicin, cell lysis with 0.2% Triton X-100 at different times p.i., and determination of CFU) was then applied. J774. A1 cells were also infected with

of *B. suis* GFP) and 1,900 \pm 300 (inoculum of *B. suis* GFP and *B. melitensis* B3B2) for experiment D. In four separate experiments, at 48 h p.i., the numbers of intracellular *B. suis* GFP cells were (i) significantly lower in coinfections than in macrophages infected with only *B. suis* GFP ($P < 0.001$ and $P < 0.01$ for experiments C and D, respectively), (ii) significantly higher in coinfections performed in the presence of L-NAME than in its absence ($P < 0.05$), and (iii) significantly higher in coinfections performed in the presence of anti-TNF- α R than in its absence ($P < 0.01$).

B. suis GFP alone (MOI = 40) or with one of the rough mutants (MOI = 40). To measure only the development of *B. suis* GFP, and not that of the rough strain, cell lysates were applied to TSA plates containing 50 µg of ampicillin per ml. *B. suis* GFP carries a stable resistance gene to this antibiotic (39), while rough *Brucella* strains did not proliferate on these plates. Figure 2A shows that the phagocytosis of *B. suis* GFP was not affected by the presence of *B. suis* manb or *B. melitensis* B3B2. In parallel, the phagocytosis of the rough strain was not modified in presence of *B. suis* (data not shown). These observations agreed with the different pathways of entry of smooth and rough *Brucella* strains (35). At 24 and 48 h p.i., the number of intracellular *B. suis* GFP organisms was significantly lower within macrophages infected with both strains than within macrophages infected with *B. suis* GFP alone (Fig. 2A). In coinfecting cells, NO₂⁻ and TNF-α accumulated in supernatants of cells simultaneously infected with *B. suis* GFP and *B. suis* manb (or *B. melitensis* B3B2), but not (or poorly for TNF-α) in *B. suis* GFP-infected cells. These accumulations were similar to those occurring in supernatants of cells solely infected by rough mutants ($P > 0.2$) (Table 2). To study whether NO and TNF-α affect the fate of *B. suis* GFP, the iNOS inhibitor L-NAME (*N*-ω-nitro-L-arginine methyl ester) (21) or a blocking anti-TNF-α receptor (TNF-αR) antibody was assessed in coinfection experiments. L-NAME does not affect the infection of J774.A1 cells with only *B. suis* (21). On the contrary, it reversed the inhibition of the intracellular development of *B. suis* GFP induced by the rough mutant and favored the growth of the pathogen (Fig. 2C). The anti-TNF-αR antibody also exerted a similar effect (Fig. 2D). The concomitant measurement of NO₂⁻ in cell supernatants confirmed the inhibitory effect of L-NAME on NO production. At 48 h p.i., NO₂⁻ concentrations in the presence and absence of L-NAME were 4.25 ± 1 and 37 ± 5 µM, respectively, in coinfections involving *B. suis* GFP and *B. melitensis* B3B2. As expected (6, 21), in control cells at 48 h p.i., L-NAME (20-fold) and the anti-TNF-αR antibody (5-fold) positively affected the development of *B. melitensis* B3B2 (data not shown). Altogether, the experiments finally indicated that TNF-α and NO resulting from a response triggered by rough bacteria inhibited the development of *B. suis* GFP. In the presence of L-NAME or anti-TNF-αR antibody, the number of *B. suis* GFP cells in coinfecting cells did not differ from that in cells infected with *B. suis* GFP alone. Therefore, when the NO or TNF-α effect is neutralized, the intracellular development of *B. suis* GFP was not affected by the presence of rough bacteria within the cells. Therefore, the inhibition of *B. suis* GFP development was not due to (i) too large an ingestion of rough bacteria by macrophages that could have damaged the cells, nor (ii) a rerouting of the bacteria towards phagolysosomes, because the level of uptake of *B. suis* was not significantly affected by the uptake of the rough strain and vice versa, a result in accordance with the different routes of entry of smooth and rough *Brucella* strains (35). Finally, the impairment of the development of *B. suis* GFP reversed by L-NAME or anti-TNF-αR resulted from a direct response of the macrophage to rough *Brucella* strains. Therefore, smooth *Brucella* strains might achieve long-term persistence, because they do not initiate the production of NO and TNF-α, two factors that induce the clearance of rough

Brucella. This may also be true for other inflammatory molecules at different stages of infection.

B. abortus binds to several different receptors, including LPS receptors (4). However, the LPS from both rough and smooth *Brucella* strains is a weak activator of macrophages (19, 26). Therefore, the elevated expression of cytokine and iNOS transcripts in rough *Brucella*-infected macrophages compared to macrophages stimulated by *E. coli* LPS could mean that the bacterial LPS is not the only molecule involved in macrophage stimulation. Such a possibility is in agreement with observations showing that TLR-2, but not TLR-4 which is involved in LPS response, mediates macrophage activation by heat killed *Brucella* (25). This should explain how rough *Brucella* strains are able to trigger the complete cell signaling pathways leading to NO production, while LPS-induced production of NO requires an additional signal given by exogenous IFN-γ (21). In accordance with previous reports comparing *B. abortus* 2308 and *B. abortus* RB51 (38), *B. melitensis* and its *whoA* mutant (13), or *B. suis* and its rough mutants (35), observations from our group indicate that many more receptors are engaged in macrophage response to rough *Brucella* infection than in response to smooth *Brucella* infection (35, 37). This could explain the potent capacity of rough mutants to stimulate macrophages. The different pathways of phagocytosis of rough and smooth bacteria suggest that these bacteria engage different sets of receptors (35). Therefore, besides the number of receptors engaged, their specificity is certainly of importance. In any case, the slight response associated with smooth *Brucella* infection indicates a mechanism by which the LPS O chain modulates the host immune response to the pathogen's advantage. Besides its properties mentioned above (13, 14, 16, 30, 32, 35, 39), this O chain characteristic must be taken into account to explain the virulence of pathogenic *Brucella*. The cell signals by which smooth *Brucella* avoids macrophage activation at the molecular level are now under investigation.

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